

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: HIRANO, TOSHIO
KAISHO, TSUNEYASU
- (ii) TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING
PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
(B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
(C) CITY: ARLINGTON
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/624,650
(B) FILING DATE: 22-MAY-1996
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/JP94/01732
(B) FILING DATE: 14-OCT-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 5-281622
(B) FILING DATE: 15-OCT-1993
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: OBLON, NORMAN F.
(B) REGISTRATION NUMBER: 24,618
(C) REFERENCE/DOCKET NUMBER: 7625-001-0 PCT
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-413-3000
(B) TELEFAX: 703-413-2220

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGGAATTCA TGGCATCTAC TTCGTATGAC TATTGCAGAG TGCCCATGGA AGACGGGGAT	60
AAGCGCTGTA AGCTTCTGCT GGGGATAGGA ATTCTGGTGC TCCTGATCAT CGTGATTCTG	120
GGGGTGCCCT TGATTATCTT CACCATCAAG GCCAACAGCG AGGCCTGCCG GGACGGCCTT	180
CGGGCAGTGA TGGAGTGTCT CAATGTCACC CATCTCCTGC AACAAAGAGCT GACCGAGGCC	240
CAGAAGGGCT TTCAGGATGT GGAGGCCCCAG GCCGCCACCT GCAACCACAC TGTGATGGCC	300
CTAATGGCTT CCCTGGATGC AGAGAAGGCC CAAGGACAAA AGAAAGTGGA GGAGCTTGAG	360
GGAGAGATCA CTACATTAAA CCATAAGCTT CAGGACGCGT CTGCAGAGGT GGAGCGACTG	420
AGAAGAGAAA ACCAGGTCTT AAGCGTGAGA ATCGCGGACA AGAAGTACTA CCCCAGCTCC	480
CAGGACTCCA GCTCCGCTGC GGCGCCCCAG CTGCTGATTG TGCTGCTGGG CCTCAGCGCT	540
CTGCTGCAGT GAGATCCCAG GAAGCTGGCA CATCTTGGA GGTCCGTCCT GCTCGGCTTT	600
TGGCTTGAAC ATTCCCTTGA TCTCATCAGT TCTGAGCGGG TCATGGGGCA ACACGGTTAG	660
CGGGGAGAGC ACGGGGTAGC CGGAGAAGGG CCTCTGGAGC AGGTCTGGAG GGGCCATGGG	720
GCAGTCCTGG GTGTGGGGAC ACAGTCGGGT TGACCCAGGG CTGTCTCCCT CCAGAGCCTC	780
CCTCCGGACA ATGAGTCCCC CCTCTTGTCT CCCACCCTGA GATTGGGCAT GGGGTGCGGT	840
GTGGGGGGCA TGTGCTGCCT GTTGTTATGG GTTTTTTTTG CGGGGGGGGT TGCTTTTTTC	900
TGGGGTCTTT GAGCTCCAAA AAATAACAC TTCCTTTGAG GGAGAGCAAA AAAAAAAAAA	960
AAAAAAAAAA AAAAAAAAAA AAAGAATTCC ACCACA	996

【 SEQUENCE TABLE】

SEQ ID NO: 1

SEQUENCE LENGTH: 180

SEQUENCE TYPE: Amino acid

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION:

Met	Ala	Ser	Thr	Ser	Tyr	Asp	Tyr	Cys	Arg	Val	Pro	Met	Glu	Asp	Gly
				5					10					15	
Asp	Lys	Arg	Cys	Lys	Leu	Leu	Leu	Gly	Ile	Gly	Ile	Leu	Val	Leu	Leu
				20					25					30	
Ile	Ile	Val	Ile	Leu	Gly	Val	Pro	Leu	Ile	Ile	Phe	Thr	Ile	Lys	Ala
				35					40					45	
Asn	Ser	Glu	Ala	Cys	Arg	Asp	Gly	Leu	Arg	Ala	Val	Met	Glu	Cys	Arg
				50					55					60	
Asn	Val	Thr	His	Leu	Leu	Gln	Gln	Glu	Leu	Thr	Glu	Ala	Gln	Lys	Gly
				65					70					75	
Phe	Gln	Asp	Val	Glu	Ala	Gln	Ala	Ala	Thr	Cys	Asn	His	Thr	Val	Met
				85					90					95	
Ala	Leu	Met	Ala	Ser	Leu	Asp	Ala	Glu	Lys	Ala	Gln	Gly	Gln	Lys	Lys
				100					105					110	
Val	Glu	Glu	Leu	Glu	Gly	Glu	Ile	Thr	Thr	Leu	Asn	His	Lys	Leu	Gln
				115					120					125	
Asp	Ala	Ser	Ala	Glu	Val	Glu	Arg	Leu	Arg	Arg	Glu	Asn	Gln	Val	Leu
				130					135					140	
Ser	Val	Arg	Ile	Ala	Asp	Lys	Lys	Tyr	Tyr	Pro	Ser	Ser	Gln	Asp	Ser
				145					150					155	
Ser	Ser	Ala	Ala	Ala	Pro	Gln	Leu	Leu	Ile	Val	Leu	Leu	Gly	Leu	Ser
				165					170					175	
Ala	Leu	Leu	Gln												

SEQ ID NO: 2
 SEQUENCE LENGTH: 996
 SEQUENCE TYPE: Nucleic acid
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE: cDNA to mRNA
 METHOD FOR DETERMINING FEATURES: E
 SEQUENCE DESCRIPTION:

GTGGAATTC ATG GCA TCT ACT TCG TAT GAC TAT TGC AGA GTG CCC ATG GAA	51
GAC GGG GAT AAG CGC TGT AAG CTT CTG CTG GGG ATA GGA ATT CTG GTG	99
CTC CTG ATC ATC GTG ATT CTG GGG GTG CCC TTG ATT ATC TTC ACC ATC	147
AAG GCC AAC AGC GAG GCC TGC CGG GAC GGC CTT CGG GCA GTG ATG GAG	195
TGT CGC AAT GTC ACC CAT CTC CTG CAA CAA GAG CTG ACC GAG GCC CAG	243
AAG GGC TTT CAG GAT GTG GAG GCC CAG GCC GCC ACC TGC AAC CAC ACT	291
GTG ATG GCC CTA ATG GCT TCC CTG GAT GCA GAG AAG GCC CAA GGA CAA	339
AAG AAA GTG GAG GAG CTT GAG GGA GAG ATC ACT ACA TTA AAC CAT AAG	387
CTT CAG GAC GCG TCT GCA GAG GTG GAG CGA CTG AGA AGA GAA AAC CAG	435
GTC TTA AGC GTG AGA ATC GCG GAC AAG AAG TAC TAC CCC AGC TCC CAG	483
GAC TCC AGC TCC GCT GCG GCG CCC CAG CTG CTG ATT GTG CTG CTG GGC	531
CTC AGC GCT CTG CTG CAG TGAGATCCCA GGAAGCTGGC ACATCTTGGA AGGTCCGTCC	589
TGCTCGGCTT TTCGCTTGAA CATTCCCTTG ATCTCATCAG TTCTGAGCGG GTCATGGGGC	649
AACACGGTTA GCGGGGAGAG CACGGGGTAG CCGGAGAAGG GCCTCTGGAG CAGGTCTGGA	709
GGGGCCATGG GGCAGTCCTG GGTGTGGGGA CACAGTCGGG TTGACCCAGG GCTGTCTCCC	769
TCCAGAGCCT CCCTCCGGAC AATGAGTCCC CCCTCTTGTC TCCCACCCTG AGATTGGGCA	829
TGGGGTGCGG TGTGGGGGGC ATGTGCTGCC TGTGTTATG GGTTTTTTTT GCGGGGGGGG	889
TTGCTTTTTT CTGGGGTCTT TGAGCTCCAA AAAATAAACA CTTCTTTTGA GGGAGAGCAA	949
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC CACCACA	996